

Fig. 1

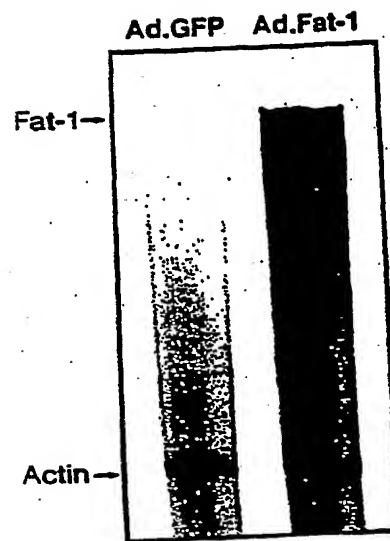


Fig. 2

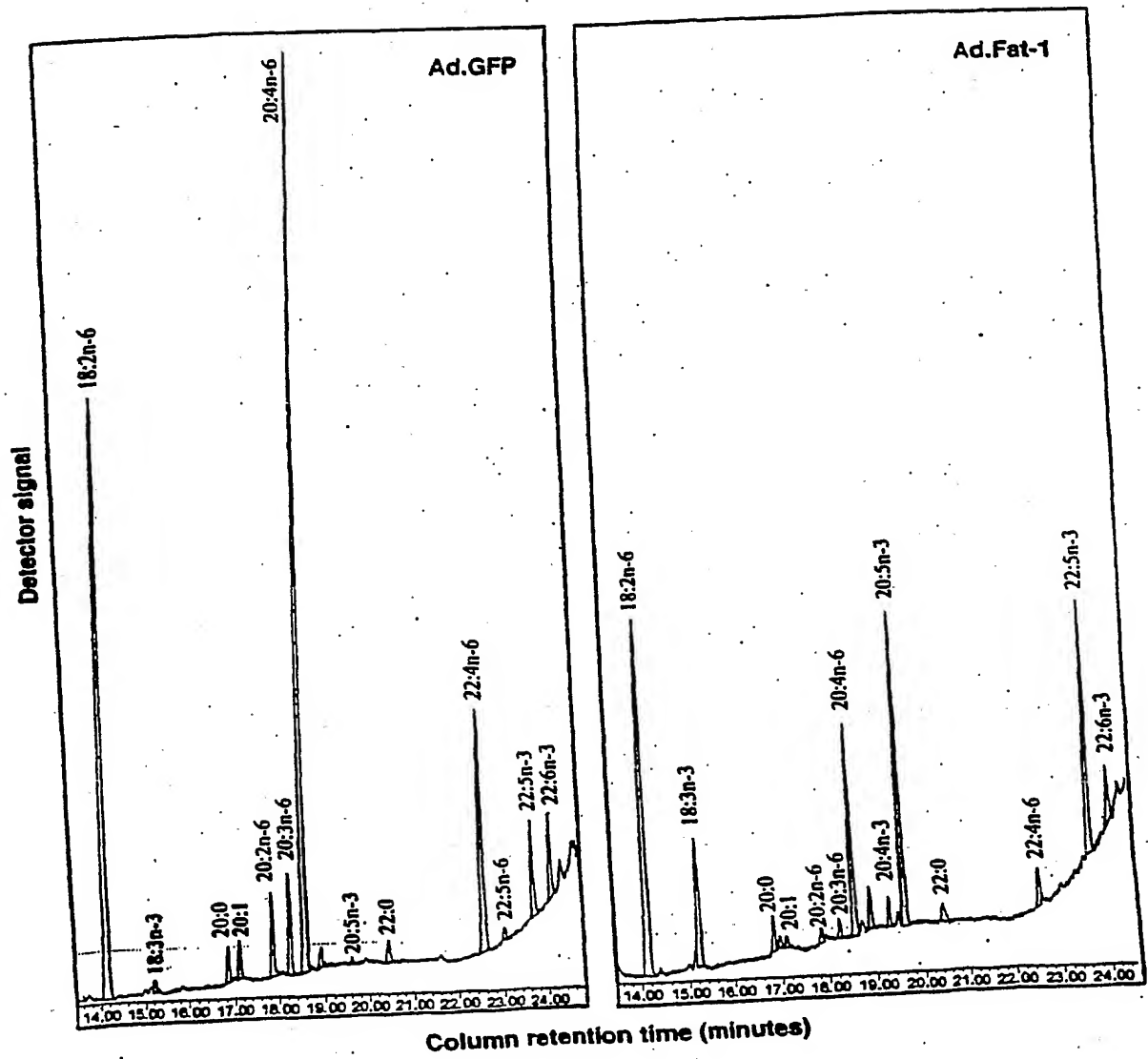


Fig. 3

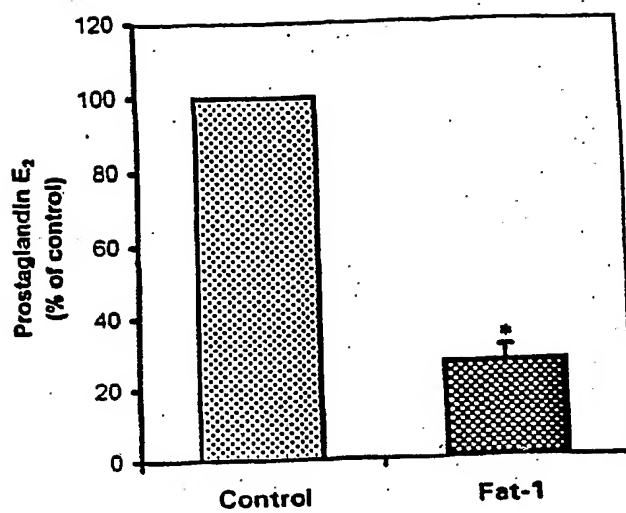


Fig. 4

Mol % of total Fatty acids	Control	Fat-1
n-6 Polyunsaturates		
18:2n-6	14.2 ^a	9.2 ^b
20:2n-6	1.2 ^a	0.3 ^b
20:3n-6	1.6 ^a	0.4 ^b
20:4n-6	15.2 ^a	4.1 ^b
22:4n-6	4.4 ^a	1.0 ^b
22:5n-6	0.2 ^a	0.0 ^b
Total	36.8 ^a	15.0 ^b
n-3 Polyunsaturates		
18:3n-3	0.2 ^b	3.6 ^a
20:4n-3	0.0 ^b	0.6 ^a
20:5n-3	0.1 ^b	6.1 ^a
22:5n-3	1.2 ^b	5.8 ^a
22:6n-3	1.0 ^a	1.3 ^a
Total	2.5 ^b	17.4 ^a
n-6/n-3 Ratio	14.7^a	0.9^b

Values are means of four measurements. Values for each fatty acid with the same letter do not differ significantly ($P < 0.01$) between control and fat-1.

Fig. 5

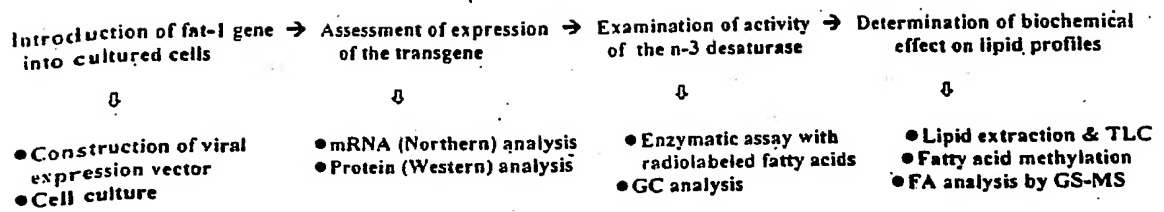


Fig. 4

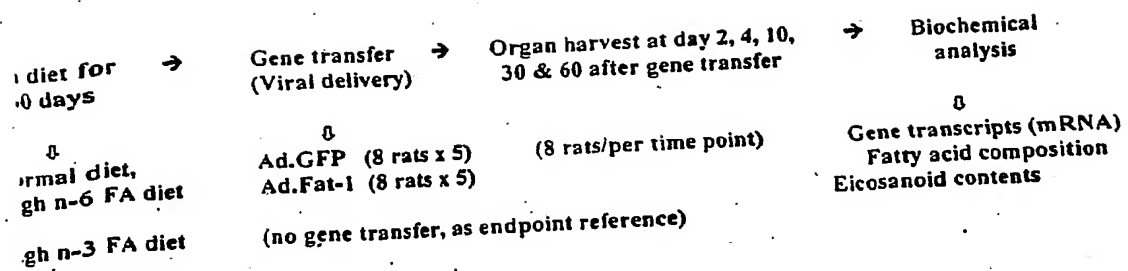


Fig. 7

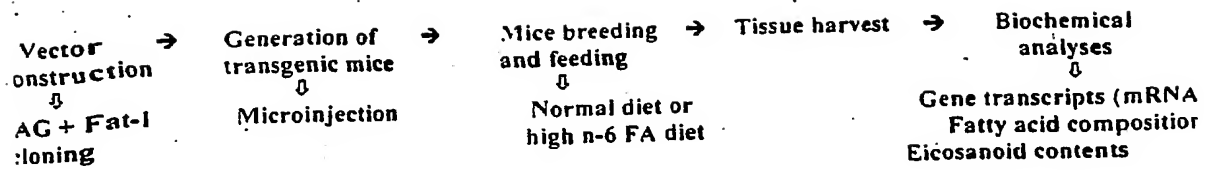


Fig. 8

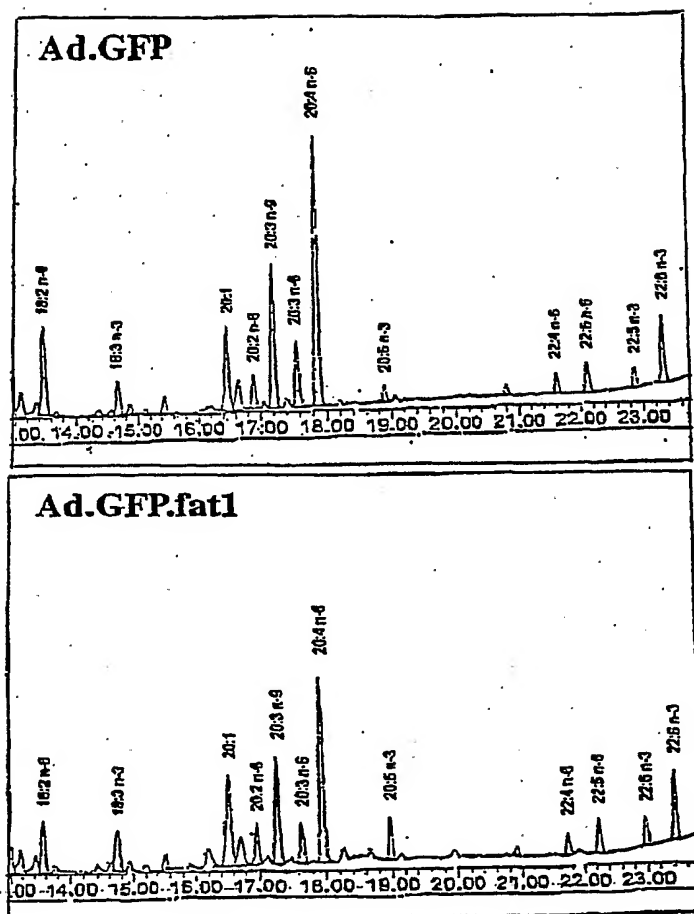


Fig. 9

PUFA composition of total cellular lipids from the control rat cortical and the transgenic cells expressing a *C. elegans fat-1* cDNA

Mol % of total fatty acids	Control	<i>fat-1</i>
n-6 Polyunsaturates		
18:2n-6	1.78	0.87
20:4n-6	7.21	4.23
22:4n-6	1.57	0.72
22:5n-6	1.68	0.72
Total	12.26	6.53
n-3 Polyunsaturates		
18:3n-3	0.34	0.86
20:5n-3	0.21	0.87
22:5n-3	0.29	0.81
22:6n-3	1.27	1.93
Total	2.11	4.48
n-6/n-3 Ratio	6.44	1.67

Values are means of four measurements. ($p < 0.01$) between control and *fat-1*.

Fig. 10

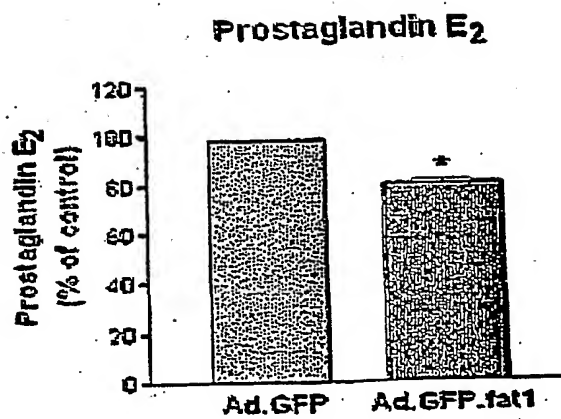


Fig. 11

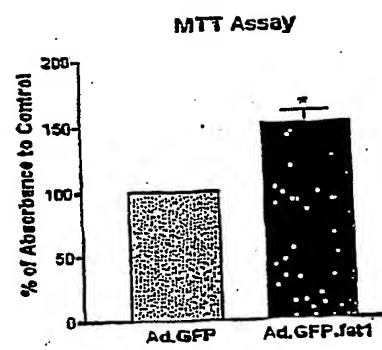
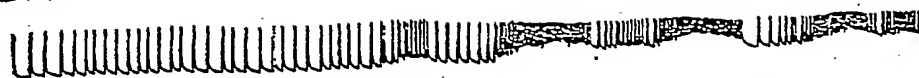


Fig. 12

Ad.GFP



$\uparrow \text{Ca}^{2+}$ (7.5mM)

Ad.GFP.Fat-1



$\uparrow \text{Ca}^{2+}$ (7.5mM)

Fig.13

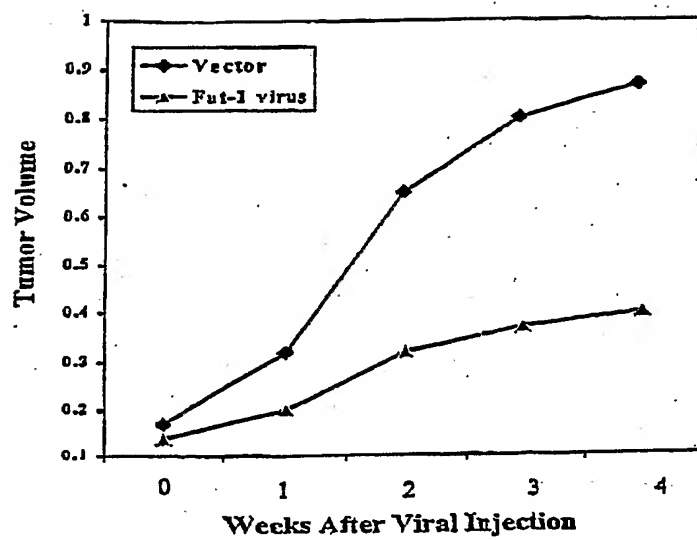


Fig. 14

PUFA composition of total cellular lipids from the control MCF-7 and the transgenic cells expressing a *C. elegans fat-1* cDNA

Mol % of total fatty acids	Control	Fat-1
n-6 Polyunsaturates		
18:2n-6	3.13 ^a	1.51 ^b
20:2n-6	0.23 ^a	0.22 ^a
20:3n-6	0.34 ^a	0.16 ^b
20:4n-6	6.30 ^a	2.26 ^b
22:4n-6	0.53 ^a	0.33 ^b
22:5n-6	0.27 ^a	0.11 ^b
Total	10.80 ^a	4.59 ^b
n-3 Polyunsaturates		
18:3n-3	0.0 ^b	1.00 ^a
20:4n-3	0.0 ^b	0.10 ^a
20:5n-3	0.0 ^b	2.87 ^a
22:5n-3	0.33 ^b	1.47 ^a
22:6n-3	0.60 ^a	0.73 ^a
Total	0.93 ^b	6.17 ^b
n-6/n-3 Ratio	11.61^a	0.74^b

Values are means of four measurements. Values for each fatty acid with the same letter do not differ significantly ($p < 0.01$) between control and fat-1.

Fig. 15

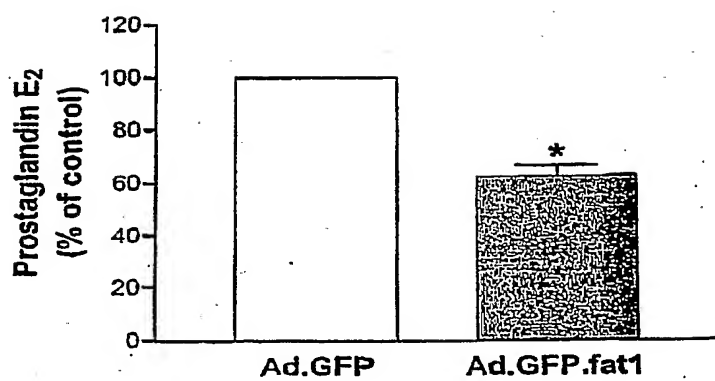


Fig. 16

17/22

CAAGTTTGAG GT

ATG GTC GCT CAT TCC TCA GAA GGG TTA TCC GCC ACG GCT CCG GTC	57
Met Val Ala His Ser Ser Glu Gly Leu Ser Ala Thr Ala Pro Val	15
5	
ACC GGC GGA GAT GTT CTG GTT GAT GCT CGT GCA TCT CTT GAA GAA	102
Thr Gly Gly Asp Val Leu Val Asp Ala Arg Ala Ser Leu Glu	30
20	
AAG GAG GCT CCA CGT GAT GTG AAT GCA AAC ACT AAA CAG GCC ACC	147
Lys Glu Ala Pro Arg Asp Val Asn Ala Asn Thr Lys Gln Ala Thr	45
35	
ACT GAA GAG CCA CGC ATC CAA TTA CCA ACT GTG GAT GCT TTC CGT	192
Thr Glu Glu Pro Arg Ile Gln Leu Pro Thr Val Asp Ala Phe Arg	60
50	
CGT GCA ATT CCA GCA CAC TGT TTC GAA AGA GAT CTC GTT AAA TCA	237
Arg Ala Ile Pro Ala His Cys Phe Glu Arg Asp Leu Val Lys Ser	75
65	
ATC AGA TAT TTG CTG CAA GAC TTT GCG GCA CTC ACA ATT CTC TAC	282
Ile Arg Tyr Leu Val Gln Asp Phe Ala Ala Leu Thr Ile Leu Tyr	90
80	
TTT GCT CTT CCA GCT TTT GAG TAC TTT GGA TTG TTT GGT TAC TTG	327
Phe Ala Leu Pro Ala Phe Glu Tyr Phe Gly Leu Phe Gly Tyr Leu	105
95	
GTT TGG AAC ATT TTT ATG GGA GTT TTT GGA TTC GCG TTG TTC GTC	372
Val Trp Asn Ile Phe Met Gly Val Phe Gly Phe Ala Leu Phe Val	120
110	
GTT GGA CAC GAT TGT CTT CAT GGA TCA TTC TCT GAT AAT CAG AAT	417
Val Gly His Asp Cys Leu His Gly Ser Phe Ser Asp Asn Gln Asn	135
125	
CTC AAT GAT TTC ATT GGA CAT ATC GCC TTC TCA CCA CTC TTC TCT	462
Leu Asn Asp Phe Ile Gly His Ile Ala Phe Ser Pro Leu Phe Ser	150
140	
CCA TAC TTC CCA TGG CAG AAA AGT CAC AAG CTT CAC CAT GCT TTC	507
Pro Tyr Phe Pro Trp Gln Lys Ser His Lys Leu His His Ala Phe	165
155	
ACC AAC CAC ATT GAC AAA GAT CAT GGA CAC GTG TGG ATT CAG GAT	552
Thr Asn His Ile Asp Lys Asp His Gly His Val Trp Ile Gln Asp	180
170	
AAG GAT TGG GAA GCA ATG CCA TCA TGG AAA AGA TGG TTC AAT CCA	597
Lys Asp Trp Glu Ala Met Pro Ser Trp Lys Arg Trp Phe Asn Pro	195
185	
ATT CCA TTC TCT GGA TGG CTT AAA TGG TTC CCA GTG TAC ACT TTA	642
Ile Pro Phe Ser Gly Trp Leu Lys Trp Phe Pro Val Tyr Thr Leu	210
200	
TTC GGT TTC TGT GAT GGA TCT CAC TTC TGG CCA TAC TCT TCA CTT	687

Fig. 17A

18/22

Phe Gly Phe Cys Asp Gly Ser His Phe Trp Pro Tyr Ser Ser Leu	
215 220 225	
TTT GTT CGT AAC TCT GAC CGT GTT CAA TGT GTA ATC TCT GGA ATC	732
Phe Val Arg Asn Ser Asp Arg Val Gln Cys Val Ile Ser Gly Ile	
230 235 240	
TGT TGC TGT GTG TGT GCA TAT ATT GCT CTA ACA ATT GCT GGA TCA	777
Cys Cys Cys Val Cys Ala Tyr Ile Ala Leu Thr Ile Ala Gly Ser	
245 250 255	
TAT TCC AAT TGG TTC TGG TAC TAT TGG GTT CCA CTT TCT TTC TTC	822
Tyr Ser Asn Trp Phe Trp Tyr Tyr Trp Val Pro Leu Ser Phe Phe	
260 265 270	
GGA TTG ATG CTC GTC ATT GTT ACC TAT TTG CAA CAT GTC GAT GAT	867
Gly Leu Met Leu Val Ile Val Thr Tyr Leu Gln His Val Asp Asp	
275 280 285	
GTC GCT GAG GTG TAC GAG GCT GAT GAA TGG AGC TTC GTC CGT GGA	912
Val Ala Glu Val Tyr Glu Ala Asp Glu Trp Ser Phe Val Arg Gly	
290 295 300	
CAA ACC CAA ACC ATC GAT CGT TAC TAT GGA CTC GGA TTG GAC ACA	957
Gln Thr Gln Thr Ile Asp Arg Tyr Tyr Gly Leu Gly Leu Asp Thr	
305 310 315	
ACG ATG CAC CAT ATC ACA GAC GGA CAC GTT GCC CAT CAC TTC TTC	1062
Thr Met His His Ile Thr Asp Gly His Val Ala His His Phe Phe	
320 325 330	
AAC AAA ATC CCA CAT TAC CAT CTC ATC GAA GCA ACC GAA GGT GTC	1047
Asn Lys Ile Pro His Tyr His Leu Ile Glu Ala Thr Glu Gly Val	
335 340 345	
AAA AAG GTC TTG GAG CCG TTG TCC GAC ACC CAA TAC GCG TAC AAA	1092
Lys Lys Val Leu Glu Pro Leu Ser Asp Thr Gln Tyr Gly Tyr Lys	
350 355 360	
TCT CAA GTG AAC TAC GAT TTC TTT GCC CGT TTC CTG TGG TTC AAC	1137
Ser Gln Val Asn Tyr Asp Phe Phe Ala Arg Phe Leu Trp Phe Asn	
365 370 375	
TAC AAG CTC GAC TAT CTC GTT CAC AAG ACC GCC GGA ATC ATG CAA	1182
Tyr Lys Leu Asp Tyr Leu Val His Lys Thr Ala Gly Ile Met Gln	
380 385 390	
TTC CGA ACA ACT CTC GAG GAG AAG GCA AAG GCC AAG TAA	1221
Phe Arg Thr Thr Leu Glu Glu Lys Ala Lys Ala Lys	
395 400	
AAGAATATCC CGTGCCGTTT TAGAGTACAA CAACAACTTC TGCGTTTTC	1271
CCGGTTTTGC TCTAATTGCA ATTTTCTTT GTTCTATATA TATTTTTTG	1321
CTTTTAAATT TTATTCTCTC TAAAAAATT CTACTTTTCA GTGCGTTGAA	1371
TGCATAAAGC CATAACTCTT	1391

Fig. 17B

Optimized 120-1 sequence

1. caa gtt tga ggt ATG gtc gct cat tcc AGC gaa ggg CtG tcc gcc acg gct ccg gtc acc
 61. ggc ggC gat gtG ctg gtG gat gcC cgt gca tct ctG gaG gaG aag gag gcC ccC cgC gaC
 121. gtg aat gca aac act aaa cag gcc acc act gaG gag ccC cgC atc caG tta ccC act gtg
 181. gat gcC ttc cgC cgC gca att ccC gca cac tgC ttc gaG agG gaC ctc gtG aaa tca atc
 241. agG tat CtG gtg caG gac ttt gcg gca ctG aca att ctG tac ttt gcC ctt ccC gcC ttt
 301. gag tac ttt ggC CtG ttt ggt tac CtG gtG tgg aac att ttt atg ggC gtt ttt ggC ttc
 361. gcg CtG ttc gtc gtt gga cac gaC tgt ctt caC ggC tca ttc tcC gat aat cag aat ctc
 421. aat gat ttc att gga cat atc gcc ttc AGC cca ctc ttc tot ccC tac ttc ccC tgg cag
 481. aaa agt cac aag ctG cac caC gcC ttc acc aac cac atC gac aaa gat cat gga cac gtg
 541. tgg atA cag gat aag gat tgg gaa gca atg ccC AGC tgg aaa aga tgg ttc aat ccT att
 601. ccT ttc tct ggC tgg ctG aaa tgg ttc ccT gtg tac act CtG ttc ggt ttc tgC gat gga
 661. tcC cac ttc tgg ccT tac tcC tca ctG ttt gtG cgC aac tct gaa cgC gtt caG tgt gta
 721. atc tct gga atc tgC tgc tgt gtg tgC gca tat att gct cta aca att gct gga AGC tat
 781. tcc aat tgg ttc tgg tac tat tgg gtt cca ctt tct ttc ttc ggC ttg atg ctc gtc att
 841. gtt acc tat CtG caG caC gtc gaC gaC gtc gct gag gtg tac gag gct gat gaa tgg agc
 901. ttc gtc cgG gga caG acc caG acc atc gat cgt tac tat ggC ctc ggC ttg gac aca acg
 961. atg cac cat atc aca gac gga cac gtt gcc caC cac ttc ttc aac aaa atc cca cat tac
 1021. cat ctc atc gaa gca acc gaa ggt gtc aaa aag gtc ttg gag ccg ttg tcc gac acc caa
 1081. tac ggg tac aaa tct caG gtg aac tac gat ttc ttt gcc cgG ttc ctg tgg ttc aac tac
 1141. aag ctc gac tat ctc gtt cac aag acc gcc gga atc atg caa ttc cga aca act ctc gag
 1201. gag aag gca aag gcc aag tGg aag aat atc ccg tgc cgt tct aga gta caa caa caa ctt
 1261. ctg cgt ttt cac cgg ttt tgc tct aat tgc aat ttt tct ttg ttc tat ata tat ttt ttt
 1321. gct ttt taa ttt tat tct ctc taa aaa act tct act ttt cag tgc gtt gaa tgc ata aag
 1381. cca taa ctc tt

Fig. 18

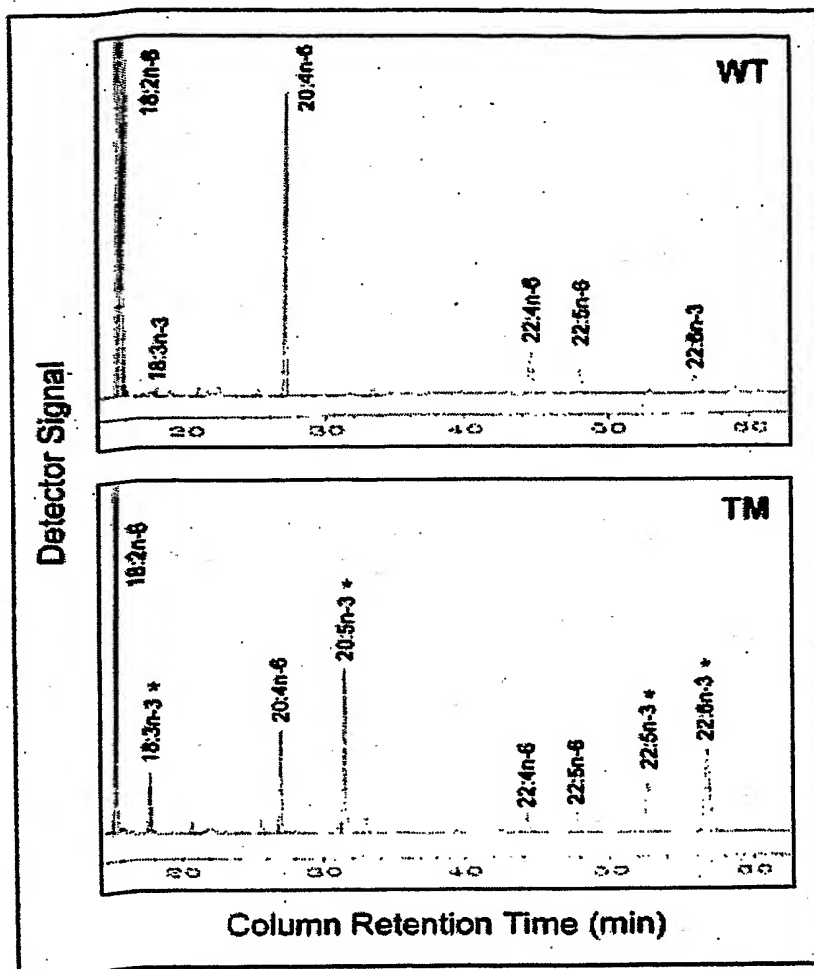


Fig. 19

Fig. 20

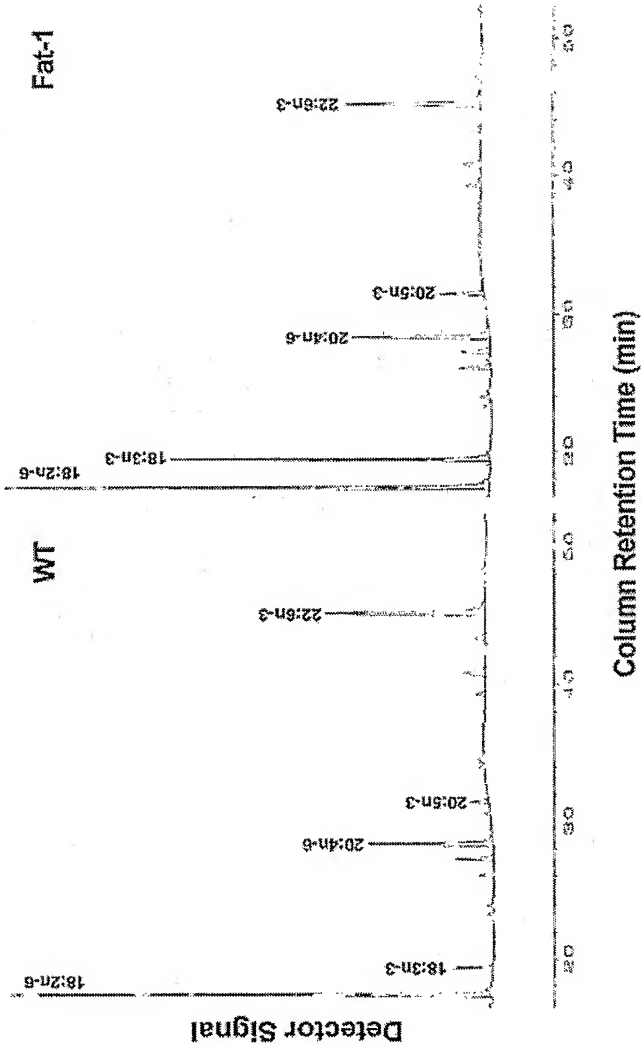


Fig. 21

